



The Global Virome Project (GVP) is an innovative 10-year partnership to detect the majority of our planet's unknown viral threats. It will pivot our approach from responding to outbreaks to proactively preparing for them. The GVP will mark the beginning of the end of the Pandemic Era.

## The Challenge

We live in an era when the threats posed by global pandemics and epidemics are greater than at any other point in human history. Recent outbreaks such as SARS, Ebola and Zika illustrate that we are ill-prepared and extremely vulnerable to emerging viral threats. However, less than 0.1% of all viruses with the potential to pose a threat to global health are estimated to have spilled over from animals to humans. Since the mid-20th century, new and deadly diseases have emerged at an alarming rate and the threats from this vast pool of unknown viruses are accelerating exponentially, driven by our expanding population and global travel.

## From Reactive to Proactive

Despite the potential impact of viral threats, the world remains unable to predict when, where, or from what species the next emerging virus will break out. To date, emphasis has been placed on reducing the impact of diseases after they have emerged – a reactive approach. Success in preventing pandemics and the uncontrolled spread of epidemics requires thinking and acting differently. Rapid and revolutionary advances in health science and technology allow us to imagine a world without the threat of novel pandemics. We must move forward to be proactive and prepare before a pandemic occurs. To achieve this, we must fill the knowledge gap for unknown viruses, including their ecology and drivers. To be fully prepared, we need to know the enemy before it emerges. The GVP will enable:

- Bioinformatics that will foster new strategies for the development of vaccines, pharmaceuticals and potentially other new classes of countermeasures *in advance* of future pandemic and epidemic events
- Strengthening of global & local capacities to monitor for and respond to viral threats while they are still evolving in animal populations to enable improved prevention of spillover

## The GVP is Transformative

The GVP is envisioned as a groundbreaking global partnership to detect and characterize virtually all of the planet's unknown viral threats circulating in animals and trigger:

**A different way of thinking:** The GVP builds on the PREDICT proof of concept and exploits advances in science and technologies to pivot our global culture from one that is reactive to one that is proactive.

**A new way of investing:** Equally importantly, the GVP challenges the global community to use this knowledge to proactively develop preventive and preparedness measures, such as vaccines and novel therapies, before spillover into human populations occurs.

## Anticipated Benefits

- Characterize the geographic scope and host range of viruses (reservoirs and transmission hosts)
- Identify behaviors and practices that potentiate spillover, allowing for the targeting of risk mitigation measures
- Monitor the movement of viruses across hosts and regions
- Establish a global surveillance network through local and global capacity enhancements (e.g. surveillance, field biology, lab proficiencies, biosafety)
- Identify transmission and pathogenicity markers for high-risk viruses
- Establish a legal, regulatory and ethical framework for sample, data, information and benefit sharing



For more information: [www.globalviromeproject.org](http://www.globalviromeproject.org)



## A Globally-Accessible Viral Atlas

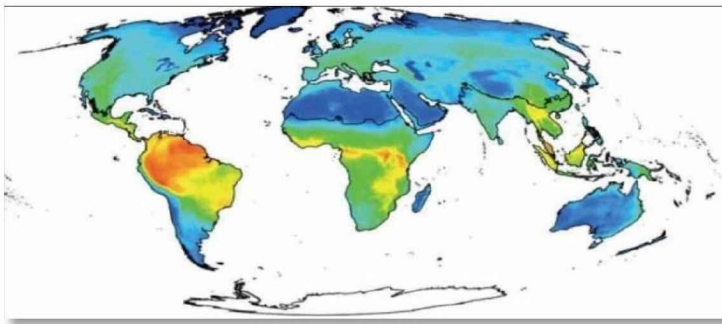
The GVP will target the vast pool of unknown future viral threats through the development of a comprehensive ecologic and genetic database of virtually all naturally-occurring viruses. Through the GVP, unknown viruses will be isolated and their sequences shared in a publicly-accessible database. Additionally, metadata on viral ecology will be collected, including host range, geographic distribution, and epidemiology. The resulting database will enable us to target high impact interventions to prevent spillover at high-risk animal-human interfaces.

## Proof of Concept

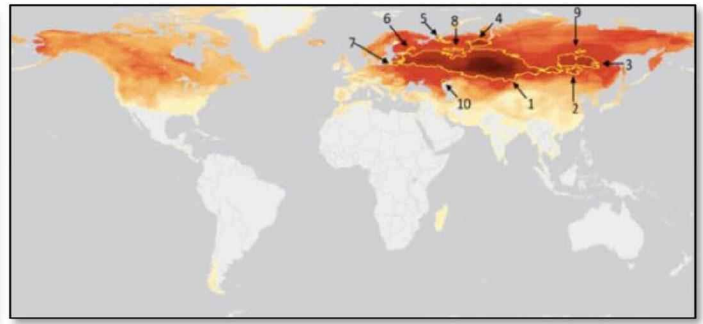
The feasibility of the GVP has been validated through USAID's PREDICT program. This viral discovery program has been operating for more than 8 years in over 30 countries, and has discovered hundreds of known and unknown viruses. PREDICT has estimated that there are over 1.3 million unknown viral species in mammalian and avian populations, of which 500,000 have the potential to infect and cause disease in humans. Based on this information, it will be possible to discover and characterize a majority of the global virome within 10 years.

### Hot Spots for Viral Diversity:

Viral diversity is closely related to mammalian diversity, allowing for geographic targeting.



*Mammalian Diversity Map: C. Rondinini et al. Phil. Trans. Roy. Soc B. 2012*



*Waterbird Diversity Map: Williamson, L., Hudson, M., O'Connell, M. et al. Biodivers Conserv (2013) 22: 1501*

## Core Principles

- Embrace an international scope, while fostering local ownership
- Promote equitable access to data and benefits
- Foster transparency
- Build national capabilities for prevention, detection and response for emerging viral threats in all partner countries on an unprecedented scale
- Foster global ownership through an international alliance

## The "Halo" Effect

In the late 1980s, the Human Genome Project catalyzed the development of new technologies and ushered in the era of personalized genomics. It is estimated that every U.S. federal dollar put into the Human Genome Project resulted in a \$178 return on investment.

The launch of the Global Virome Project is expected to yield similar benefits by accelerating the development of new diagnostics, vaccine technologies and risk mitigation strategies against emerging viral diseases. This initiative will provide a wealth of publicly accessible unbiased data, leading to advances in science and global health.

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"MAN CAN LEARN NOTHING EXCEPT BY GOING FROM THE KNOWN TO THE UNKNOWN." –CLAUDE BERNARD



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